IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Beachy, et al.

Serial No: 09/943,641

Filed: August 30, 2001

For: Identification of Activated Receptors and Ion Channels

Art Unit: 1632

Attorney Docket No. JHUC-P01-017

Examiner: To be assigned

COPY OF PAPERS ORIGINALLY FILED

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PRELIMINARY AMENDMENT

Sir:

Please enter the following amendments:

In the specification:

On page 33, please replace the third full paragraph with the following text:

Some aspects of Gα structure are relevant to the design of modified Gα subunits. The amino terminal 66 residues of GPA1 are aligned with the cognate domains of human Gαs, Gαi2, Gαi3, Gα16 and transducin. In the GPA41Gα hybrids, the amino terminal 41 residues (derived from GPA1) are identical, end with the sequence-LEKQRDKNE- (SEQ ID NO: 1) and are underlined for emphasis. All residues following the glutamate (E) residue at position 41 are contributed by the human Gα subunits, including the consensus nucleotide binding motif -GxGxxG-. Periods in the sequences indicate gaps that have been introduced to maximize alignments in this region. Codon bias is mammalian. For alignments of the entire coding regions of GPA1 with Gαs, Gαi, and Gαo, Gαq and Gαz, see Dietzel and Kurjan (Cell 50: 573, 1987) and Lambright et al. (Nature 369: 621-628, 1994). Additional sequence information is provided by Mattera et al. (FEBS Lett 206: 36-41, 1986), Bray et al. (Proc. Natl. Acad. Sci. USA 83: 8893-8897, 1986) and Bray et al. (Proc. Natl. Acad. Sci. USA 84: 5115-5119, 1987).